

CTGA: the database for genetic disorders in Arab populations

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Received July 4, 2005; Revised and Accepted September 17, 2005

ABSTRACT

The Arabs comprise a genetically heterogeneous group that resulted from the admixture of different populations throughout history. They share many common characteristics responsible for a considerable proportion of perinatal and neonatal mortalities. To this end, the Centre for Arab Genomic Studies (CAGS) launched a pilot project to construct the 'Catalogue of Transmission Genetics in Arabs' (CTGA) database for genetic disorders in Arabs. Information in CTGA is drawn from published research and mined hospital records. The database offers web-based basic and advanced search approaches. In either case, the final search result is a detailed HTML record that includes text-, URL- and graphic-based fields. At present, CTGA hosts entries for 692 phenotypes and 235 related genes described in Arab individuals. Of these, 213 phenotypic descriptions and 22 related genes were observed in the Arab population of the United Arab Emirates (UAE). These results emphasize the role of CTGA as an essential tool to promote scientific research on genetic disorders in the region. The priority of CTGA is to provide timely information on the occurrence of genetic disorders in Arab individuals. It is anticipated that data from Arab countries other than the UAE will be exhaustively searched and incorporated in CTGA (<http://www.cags.org.ae>).

INTRODUCTION

The Arabs, comprising of 315 million individuals, are living in regions encompassing Mesopotamia, Middle East, Arabian Gulf, North Africa and parts of East and West Africa. In addition, Arab diasporas, with an estimated size of 30 million people, are encountered in all over the world. Although, Arabs consist of heterogeneous groups and many isolates, they share many common characteristics with important influence on their genetic constitution. These include: high rates of

inbreeding or consanguineous marriage, elevated birth rates, child bearing in older maternal age and lack of public health measures directed at the control and prevention of congenital and genetically determined disorders (1). All these factors make genetic and congenital disorders responsible for a considerable proportion of perinatal and neonatal mortalities in Arab populations. In fact, congenital malformations are the second leading cause of infant mortality in Bahrain, Kuwait, Oman and Qatar and are the leading cause of infant mortality (40.3%) in the United Arab Emirates [UAE; (2,3)].

Since the 1950s, Arab countries have made progress in medical services leading to better life expectancies and access to health care. Similarly, Arab scholars working in the field of biomedical sciences are giving more attention to publish their results at national or international levels (4). Concurrently, several attempts to review different aspects of genetic diseases in Arab populations were conducted (5–8). However, data were rapidly outdated as new disorders were described in Arabs. To this end, the Centre for Arab Genomic Studies (CAGS) launched a pilot project to construct the 'Catalogue of Transmission Genetics in Arabs' (CTGA) database for genetic disorders in Arabs to educate the medical community and raise public awareness in at-risk populations.

SOURCE OF INFORMATION

In accordance with its objective to alleviate human suffering from genetic diseases in the Arab World, CAGS coordinated the collection of data on genetic disorders in the UAE population as a model system to be implemented in other Arab countries in the future. Information in CTGA was drawn from two main sources:

- (i) Nationally and internationally published literature: Bibliographic databases were screened for relevant articles on genetic disorders in the UAE. Whenever possible, comprehensive manual scan of hardcopies of national peer-reviewed journals was conducted.
- (ii) Laboratory records: In major hospitals of the UAE, patient records covering the last 10–15 years were studied prospectively. These hospitals included laboratories for molecular diagnostics, cytogenetics, biochemistry and

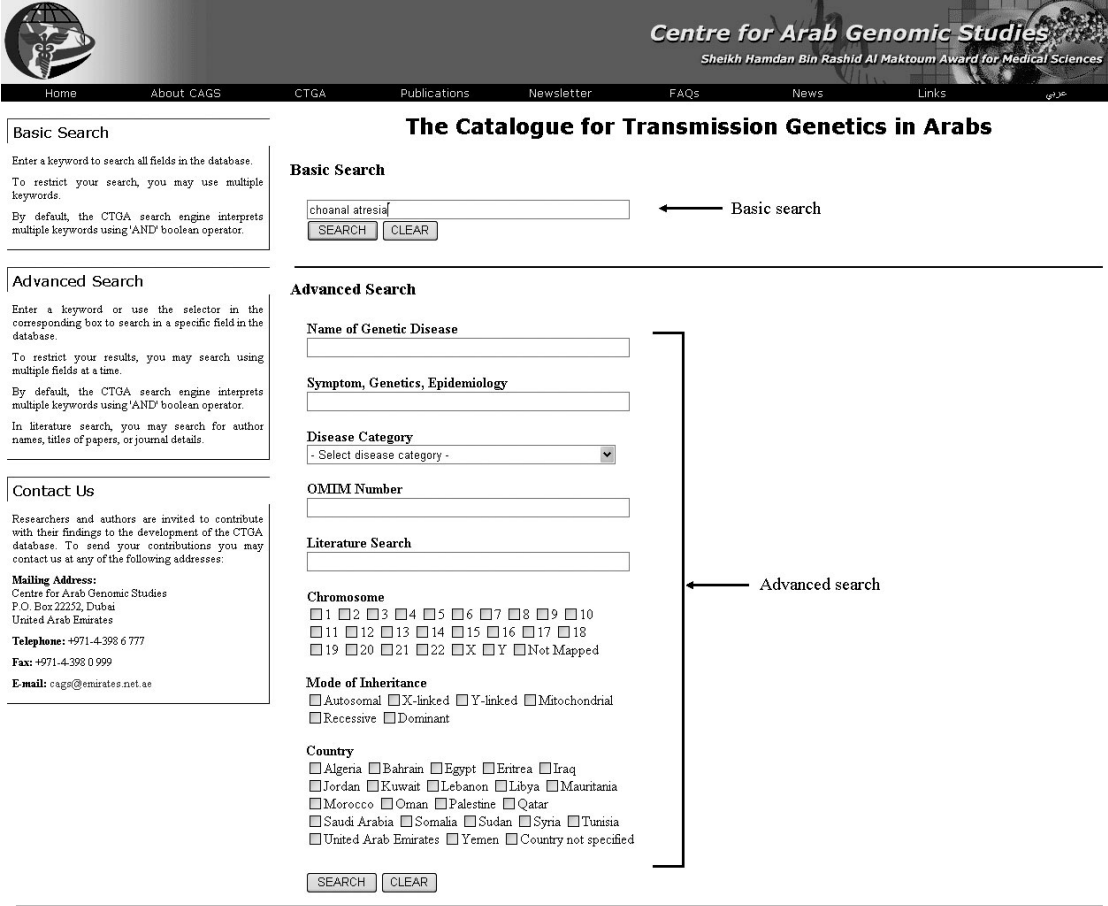
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others (1). Detailed information, including the mutation, was recorded using a standardized method. Patient records prove to be an invaluable source of information since they indicated the presence of several inherited disorders for which occurrence data had not been published before.

While data on genetic disorders in patients of various nationalities were collected, only those obtained from UAE

nationals and other Arab patients appear in the CTGA database. Furthermore, personal communication with local geneticists provided further insight into the spectrum of inherited disorders in the UAE. Succinctly, the magnitude of genetic disorders and congenital abnormalities reported from the Arab population of the UAE alone (at least 200) demonstrates the efficacy of the algorithm adapted when compared to a review on the subject (9).

(a)



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The Catalogue for Transmission Genetics in Arabs

Basic Search

Enter a keyword to search all fields in the database.
To restrict your search, you may use multiple keywords.
By default, the CTGA search engine interprets multiple keywords using 'AND' boolean operator.

choanal atresia

SEARCH CLEAR

Advanced Search

Name of Genetic Disease

Symptom, Genetics, Epidemiology

Disease Category
- Select disease category -

OMIM Number

Literature Search

Chromosome
☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☐ 8 ☐ 9 ☐ 10
☐ 11 ☐ 12 ☐ 13 ☐ 14 ☐ 15 ☐ 16 ☐ 17 ☐ 18
☐ 19 ☐ 20 ☐ 21 ☐ 22 ☐ X ☐ Y ☐ Not Mapped

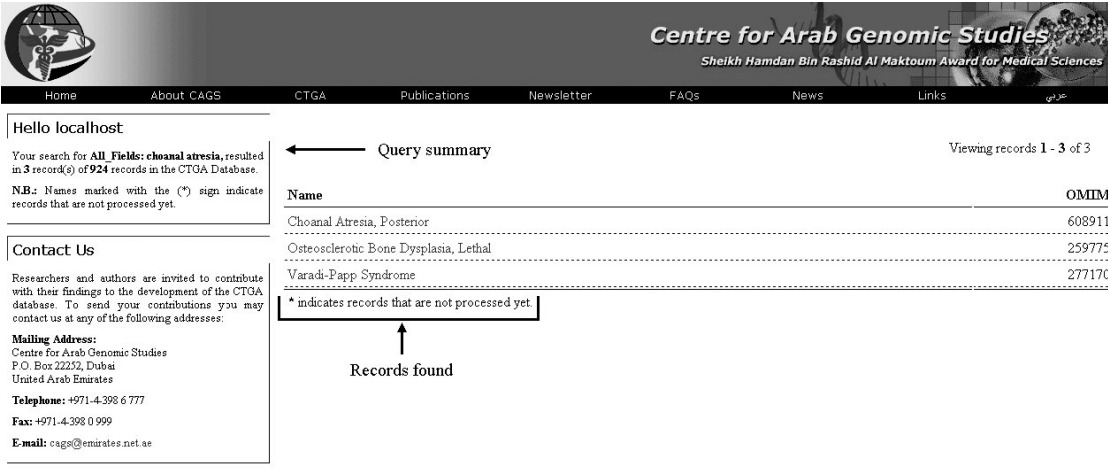
Mode of Inheritance
☐ Autosomal ☐ X-linked ☐ Y-linked ☐ Mitochondrial
☐ Recessive ☐ Dominant

Country
☐ Algeria ☐ Bahrain ☐ Egypt ☐ Entrea ☐ Iraq
☐ Jordan ☐ Kuwait ☐ Lebanon ☐ Libya ☐ Mauritania
☐ Morocco ☐ Oman ☐ Palestine ☐ Qatar
☐ Saudi Arabia ☐ Somalia ☐ Sudan ☐ Syria ☐ Tunisia
☐ United Arab Emirates ☐ Yemen ☐ Country not specified

SEARCH CLEAR

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(b)



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Hello localhost

Your search for All Fields: choanal atresia, resulted in 3 record(s) of 924 records in the CTGA Database.
N.B.: Names marked with the (*) sign indicate records that are not processed yet.

Contact Us

Researchers and authors are invited to contribute with their findings to the development of the CTGA database. To send your contributions you may contact us at any of the following addresses:

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Query summary

Viewing records 1 - 3 of 3

Name	OMIM
Choanal Atresia, Posterior	608911
Osteosclerotic Bone Dysplasia, Lethal	259775
Varadi-Papp Syndrome	277170

* indicates records that are not processed yet.

Records found

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Choanal Atresia, Posterior

Alternative Names
PCA

WHO International Classification of Diseases
Congenital malformations, deformations and chromosomal abnormalities > Congenital malformations of the respiratory system

OMIM Number
608911

Gene Map Locus
?

Mode of Inheritance
Probably a multifactorial trait, autosomal recessive inheritance also reported

Description
Choanal atresia is a rare developmental anomaly characterized by failure of communication of the posterior nasal cavity with the nasopharynx. It may be complete or incomplete, unilateral (60%) or bilateral (40%), bony (90%) or membranous (10%) or a combination of these.

The anomaly presents either immediately after birth as respiratory distress, or as a coincidental finding at an older age. The condition is the most common nasal abnormality, affecting in 1 out of every 7,000 to 8,000 live births, with a 2:1 female-to-male ratio.

Epidemiology in the Arab World

Egypt
Sadek (1998) reported two females from a consanguineous family from Egypt with bilateral congenital choanal atresia. The patients also presented features of vitamin D resistant rickets. Their mother had beta-thalassemia minor.

Al-Gazali et al. (2003) reported a male infant from unrelated Egyptian parents, residents of the United Arab Emirates, with Raine syndrome. There were no histories of any congenital anomaly or genetic disease or of maternal drug intake during pregnancy. Prenatal ultrasound showed polyhydramnios and short limbs. The baby presented at birth with severe craniofacial anomalies including a wide anterior fontanel, exophthalmos, severe depression of the nasal bridge with a hypoplastic midface, bilateral choanal atresia, and a large protruding tongue.

Palestine
Gershoni-Baruch (1992) described a small inbred Moslem kindred from Palestine in which non-syndromal choanal atresia occurred in two sibs and their paternal uncle. In a note added in proof, she reported the birth of a third affected sib.

Al-Gazali et al. (2002) reported a brother and sister from an inbred Palestinian family with an autosomal recessive syndrome of choanal atresia, hypothelia/athelia, and thyroid gland anomalies. The parents were first cousins and their first couple was a female with bilateral choanal atresia who died few hours after birth. There was a history of two miscarriages at two months of gestation. The parents and four children were normal. The male patient had, at birth, a unilateral right choanal atresia, low set ears, hypoplastic nipples, and absent breast tissue. The affected sister cried immediately after birth but three minutes later collapsed and needed incubation and resuscitation. She had widely spaced eyes with depressed nasal bridge, dysmorphic low set right ear, a small pit on the upper right side of the neck, sparse eyebrows, and long eyelashes. Both nipples were hypoplastic and there was no breast tissue. She had bilateral choanal atresia. Chromosome study was normal. She died at 4 months of age following a pneumonia. Al-Gazali et al. (2002) noted that the features overlapped those of Bamforth syndrome, hypohidrotic ectodermal dysplasia with hypothyroidism and ciliary dyskinesia (HEDH) syndrome, and methimazole embryopathy.

Syria
Sadek (1998) reported a Syrian male with bilateral congenital choanal atresia. The patient also presented features of congenital inguinal hernia and bilateral pre-auricular sinuses. His parents were second cousins and he had one brother with bilateral congenital choanal atresia. Two more brothers and three sisters were all normal.

United Arab Emirates
Sadek (1998) reported a male from the United Arab Emirates with bilateral congenital choanal atresia. The patient was born to first cousin parents who were clinically normal. His mother had five spontaneous abortions at 12 weeks, two babies who died at 5 months of age from congenital hydronephrosis, and two still births at 8 months gestation with multiple congenital anomalies. He also had a sister with unilateral choanal atresia.

Yemen
In an inbred Yemenite family, Qazi et al. (1982) observed posterior choanal atresia in a brother and sister and their paternal aunt. All four parents of the three affected persons traced to a common ancestral couple 2-3 generations earlier. In 1998, Sadek reported two males and one female from a non-consanguineous Yemeni family with bilateral congenital choanal atresia. The patients and their mother all had features of Crouzon syndrome. There were three normal siblings in the family (two brothers and one sister). [See also: Palestine > Al-Gazali et al., 2002].

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Related CTGA Records

- Osteosclerotic Bone Dysplasia, Lethal, CTGA # 34245

Links
<http://www.childsdoc.org/fall98/choanal/choanal.asp>
<http://www.emedicine.com/ent/topic330.htm>
<http://www.nlm.nih.gov/medlineplus/ency/article/001642.htm>

Contributors
Ghazi O. Tadmouri: 14.5.2005

Edit History
Sarah: 15.5.2005

Med. Sea	Tunisia	Med. Sea	Lebanon	Syria	Iraq	
				X		
Morocco	Algeria	Libya	Egypt	Palestine	Jordan	Ramot
			X	X		
Mauritania			Sudan	Sat	KSA	Pakistan
						Qatar
			Eritrea	Sea	Yemen	Oman
					X	
						UAE
						X

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Figure 1. The online layouts of the CTGA database: (a) Search, (b) results and (c) details.

THE CTGA DATABASE

The current version of CTGA is a textual database whose structure depends on a web-based search that uses an indexing system for rapid mining of information. As the retrieval

of information from the CTGA database is as important as filling data in, we paid considerable attention to provide the users with the option of performing complicated queries to obtain specific results without sacrificing the simplicity. At present, the CTGA database (<http://www.cags.org.ae>)

can be queried using two modes of search: basic or advanced. In basic search, there is a standard query box in which the user may enter one or more keywords. By default, the CTGA search engine permits the use of wildcards and automatically processes multiple keywords with the 'AND' Boolean operator. However, the power of querying at CTGA lies in its advanced search features. At this point, the user can employ a multitude of user-friendly search combinations according to the name of disease, its classification, symptoms, related gene loci, OMIM number, chromosome location, mode of inheritance, geographic location and others. Proper use of advanced search inevitably increases specificity and narrows down results to a small number of relevant records (Figure 1).

In both types of search, the user issues a command that is interpreted in the CTGA server, processed by the system's language, and results are sent to the user's browser as a standard HTML document with no requirement for any additional software. Query results are alphabetically listed in table form and include the names and corresponding OMIM numbers of genes and genetic disorders described in the Arab people. By selecting a name in the table of results, the user is able to access extensive details relating to a specific gene or genetic disorder (Figure 1).

A detailed record includes text-, URL- and graphic-based fields. The title and alternative names indicate the primary title and alternative titles and symbols of the disorder or gene. A graphical map demonstrates the geographical origin of the individuals described in the entry. A disorder is categorized according to the World Health Organization International Classification of Disease (WHO-ICD) 10th revision. OMIM number is a URL-based field that takes the user to the corresponding file of the gene or disorder at the Online Mendelian Inheritance in Man (OMIM) database (10). Information regarding Gene Map Locus is drawn primarily from OMIM. Mode of Inheritance, Description and Molecular Genetics are textual fields that contain summaries on the clinical features and genetic pathology for the corresponding entry. Epidemiology in the Arab World is the major part of an entry since it includes a detailed review of research analyses regarding the gene loci or clinical phenotypes in Arab individuals. References within an entry are linked to their corresponding PubMed abstracts except for articles from national peer-reviewed medical journals not indexed in PubMed. Following the references are two URL-based fields. Related CTGA Records takes the user to any intra-CTGA entry(ies) with a shared relationship(s) while Links anchors at external resources with additional information. Authors who contribute with additions or changes to the entry are given credit in the Contributors field along with the date when the contribution was submitted. Changes made by the editorial staff are documented in the Edit History field (Figure 1).

As of October 1 2005, CTGA had 692 phenotype entries and 235 related gene entries with descriptions in Arab individuals. In the UAE, CTGA information includes about 213 phenotypic descriptions (including 14 in Arab non-UAE nationals) and 22 related genes (including 3 in Arab non-UAE nationals). Currently, authors at the Centre for Arab Genomic Studies create about 25 entries and update an equivalent number each month. Although CTGA has a short lifespan on the public domain of the Internet, it averages at least 150 unique users per day. The peak of simultaneous users

accessing the database usually occurs between 03:00 and 12:00 GMT.

SIGNIFICANCE OF CTGA

A tool for decision-making in health-related domains

The geographical distributions of genetic disorders in CTGA can either be restricted to small locales (Stuve–Wiedemann syndrome), commonly widespread (beta-thalassemia), or reflect a patchy distribution (alpha-thalassemia) although a high prevalence is expected in the region (1). On the other hand, the molecular/biochemical pathologies in ~25% of genetic disorders described in Arabs have not been determined yet, thus, these serve as excellent candidates for linkage analyses and genotype/phenotype studies (1). Obviously, the interpretation of these data is an important tool for authorities to decide on future health-related strategies and to propose research directions on disorders for which information is still scant.

A hub of locally produced scientific information on genetic disorders

Current data on genetic disorders in CTGA reflect a bias in the geographical distribution. At present, genetic disorders recorded in Tunisia, Lebanon, Morocco and Saudi Arabia add up to ~40% of all genetic disorders in Arab populations. The main reason for this is the well-established custom of scientific reporting at international level, while in other Arab countries reports mostly appear in national publications or stay confined to non-public laboratory records (11). Consequently, by publishing scientific information locally produced in peer-reviewed journals and unpublished data collected from records of laboratories from the Arab World, CTGA exposes valuable local information that is not accessible to the large scientific community.

A catalyst for establishing collaborations with Arab scientific groups

The extended consanguineous family structure, commonly present in Arab societies, is an important factor leading to the propensity of severe congenital inherited diseases in most Arab populations (1). Incidentally, genetic disorders in Arabs tend to display peculiar distribution patterns not present in many other world populations. A major model that explains this concept is the vertical dissemination of a genetic mutation in an Arab family, where mutation carriers mostly remain concentrated within the extended family; thus, offering great opportunities to depict the genetic nature of their disease predisposition (1). In view of all the above, the wealth of information that CTGA is accumulating is, in our opinion, an indispensable tool for scientists to recognize Arab colleagues working on similar domains and decide on possible collaborations or exchange of know-how.

An educational tool on genetic disorders in the region

Studies have clearly indicated that the correct dissemination of knowledge is an important step towards the eradication of genetic disorders in Arab populations (12). The CTGA

database plays such an educational role as it addresses both the medical communities and at-risk populations.

FUTURE OF CTGA

The priority of CTGA is to provide timely information on the occurrence of genetic disorders in the Arab populations. It is anticipated that data from Arab countries other than the UAE will soon be exhaustively searched and incorporated in CTGA. A similar strategy to that applied in the UAE will be adapted using published and unpublished information. In this regard, CAGS is currently forming a council of Arab geneticists to orchestrate data collection from their corresponding countries. Besides, all geneticists working on genetic disorders in Arabs are hailed to contribute to the growth of CTGA.

On the other hand, CAGS is planning to develop CTGA into a data mart that collects information from different specialized databases using relational data models of database management systems (DBMS). These specialized databases may include DNA sequence data, mutations, polymorphisms or disorder-specific information. Certainly, such integration will add new benefits and uses of CTGA, the credence of which is simply defined by the feedback received from the database users.

ACKNOWLEDGEMENTS

The Centre for Arab Genomic Studies is a division of H.H. Sheikh Hamdan Bin Rashid Al Maktoum Award for Medical Sciences. Funding is provided by Sheikh Hamdan Bin Rashid Al Maktoum Award for Medical Sciences. We thank the Executive Committee Members of CAGS and colleagues in the various medical and academic centers who facilitated data

collection in the UAE. The authors wish to thank Dr Erol Baysal for reviewing the material for this manuscript and for providing insightful comments and suggestions. Funding to pay the Open Access publication charges for this article was provided by the Centre for Arab Genomic Studies.

Conflict of interest statement. None declared.

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